

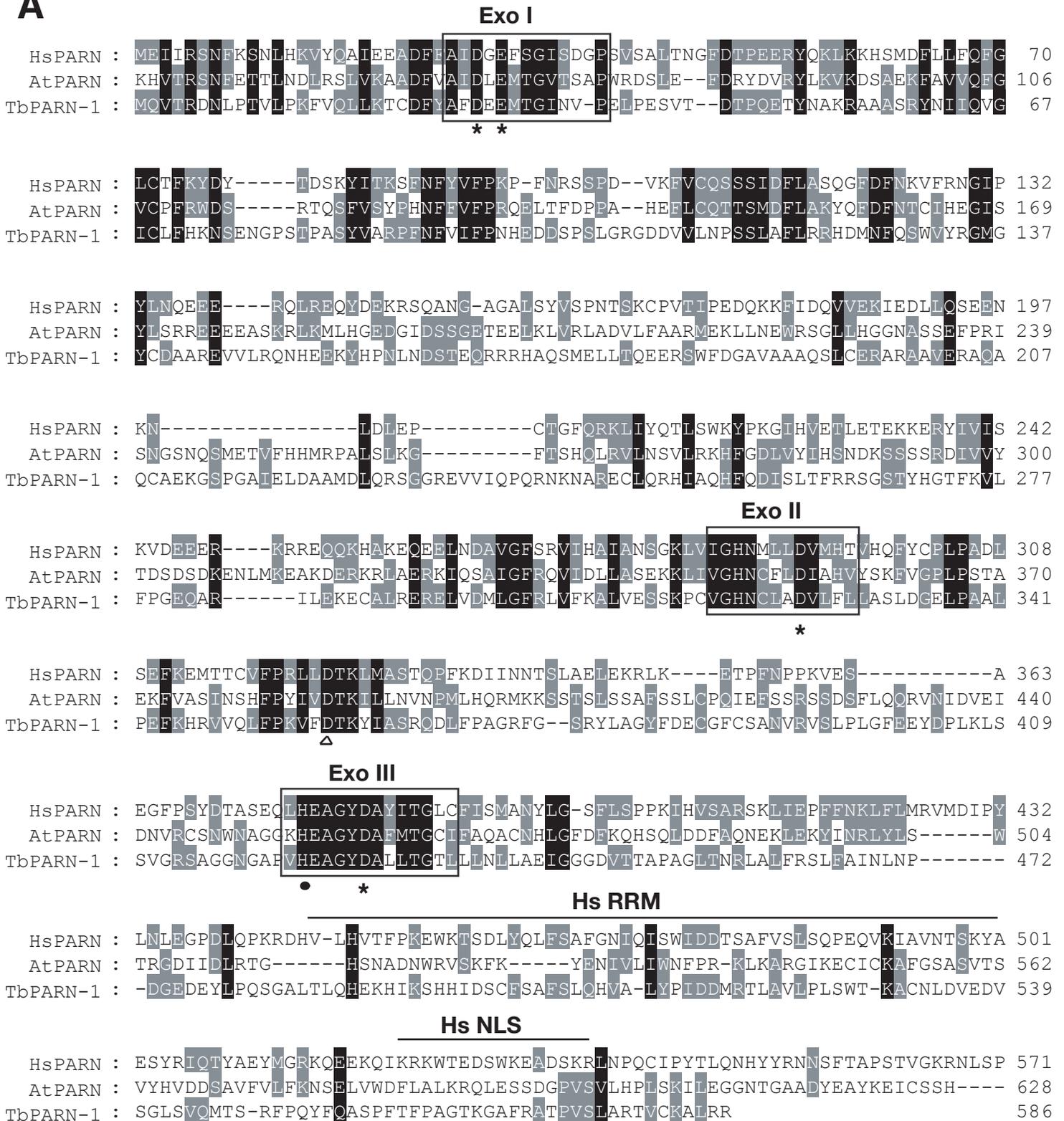
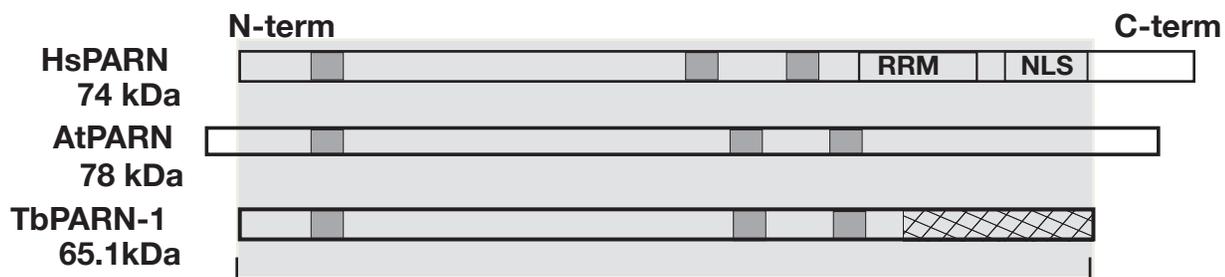
A**B****Figure S1**

Figure S1. Alignment of *T. brucei* PARN-1 (TbPARN-1), human PARN (HsPARN), and *Arabidopsis thaliana* PARN (AtPARN).

(A) Amino acid sequences are aligned to illustrate comparisons among the three proteins. The characteristic Exo I, Exo II, and Exo III motifs are boxed and the four residues of the DEDD motif required for catalytic activity are noted with *. A fifth conserved aspartate residue is shown by a Δ . The filled circle indicates the histidine in Exo III indicative of a DEDDh subfamily member (59). Grey boxes show similar amino acids in two sequences, black boxes show similar amino acids in all three sequences. The TbPARNs as well as the AtPARN proteins diverge from each other and from the HsPARN after the Exo III domain. The precise C-terminus of TbPARN is shown; AtPARN extends ~40 amino acids and HsPARN protein extends ~70 amino acids C-terminal to the sequences shown [see schematic in (B)]. The two RNA recognition motifs (RRMs) and the nuclear localization signal (NLS) present in HsPARN is absent in the AtPARN and the TbPARN proteins and are thus not shown. Accession numbers are: *Homo sapiens* (AAH50029); *Arabidopsis thaliana* (Q9LG26; At1g55870); *T. brucei* (Tb927.8.2850). The human nuclear localization signal (NLS) and RNA recognition motif (RRM) sequences are indicated. **(B)** Schematic of the HsPARN, AtPARN, and TbPARN-1 proteins. The shaded region signifies the region of the protein sequence shown in (A). The RRM and NLS present only in HsPARN are indicated. Humans and *Arabidopsis* contain a single PARN gene. *Arabidopsis* contains a second PARN-like ORF (At3g25430) that lacks the four highly conserved acidic amino acids necessary for catalysis (48).